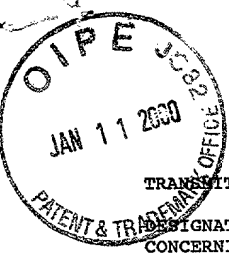


09/462629 PCT  
520 Rec'd PCT/PTO 11 JAN 2000



TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. 371

ATTORNEY'S DOCKET NUMBER 48141

U.S. APPLICATION NO. (If known, see 37 CFR 1.5)

INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/EP 98/03832	23 June 1998	14 July 1997

TITLE OF INVENTION: DNA SEQUENCE ENCODING A HYDROXYPHENYLPYRUVATE DIOXYGENASE, AND ITS OVERPRODUCTION IN PLANTS  
APPLICANT(S) FOR DO/EO/US Harald SEULBERGER, Jens LERCL, Ralf-Michael SCHMIDT, Karin KRUPINSKA, Jon FALK

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. /X/ This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.
2. / / This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.
3. /X/ This express request to begin national examination procedures (35 U.S.C.371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. /x / A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. /X/ A copy of the International Application as filed (35 U.S.C. 371(c)(2)).
  - a./X/ is transmitted herewith (required only if not transmitted by the International Bureau).
  - b./ / has been transmitted by the International Bureau.
  - c./ / is not required, as the application was filed in the United States Receiving Office (RO/USO).
6. /X/ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. / / Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)).
  - a./ / are transmitted herewith (required only if not transmitted by the International Bureau).
  - b./ / have been transmitted by the International Bureau.
  - c./ / have not been made; however, the time limit for making such amendments has NOT expired.
  - d./ / have not been made and will not be made.
8. / / A translation of the amendments to the claims under PCT Article 19(35 U.S.C. 371(c)(3)).
9. /X/ An oath or declaration of the inventor(s)(35 U.S.C. 171(c)(4)).
10. / / A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).
- Items 11. to 16. below concern other document(s) or information included:
  11. / / An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
  12. /X/ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
  13. /X/ A FIRST preliminary amendment.  
/ / A SECOND or SUBSEQUENT preliminary amendment.
  14. / / A substitute specification.
  15. / / A change of power of attorney and/or address letter.
  16. /x / Other items or information.  
International Search Report  
International Preliminary Examination Report

U.S. App'n. No. (if known) **09/462629**INTERNATIONAL APPLN. NO.  
PCT/EP 98/03832ATTORNEY'S DOCKET NO.  
48141

		CALCULATIONS	PTO USE ONLY
17. /X/ The following fees are submitted			
BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)):			
Search Report has been prepared by the			
EPO or JPO.....	\$840.00	840.00	
International preliminary examination fee paid to USPTO			
(37 CFR 1.482).....	\$750.00		
No international preliminary examination fee paid to			
USPTO (37 CFR 1.482) but international search fee paid			
to USPTO (37 CFR 1.445(a)(2)).....\$700.00			
Neither international preliminary examination fee			
(37 CFR 1.482) nor international search fee			
(37 CFR 1.445(a)(2)) paid to USPTO .....\$ 970.00			
International preliminary examination fee paid to			
USPTO (37 CFR 1.482) and all claims satisfied pro			
-visions of PCT Article 33(2)-(4).....\$96.00			
ENTER APPROPRIATE BASIC FEE AMOUNT =		\$ 840.00	
Surcharge of \$130.00 for furnishing the oath or declaration			
later than / / 20 / /30 months from the earliest			
claimed priority date (37 CFR 1.492(e)).			
<u>Claims</u>	<u>Number Filed</u>	<u>Number Extra</u>	<u>Rate</u>
Total Claims	24 -20	4	X\$18. 72.00
Indep.Claims	2 -3		X\$78.
Multiple dependent claim(s)(if applicable)			+270.
TOTAL OF ABOVE CALCULATION			= 840.00
Reduction of 1/2 for filing by small entity, if applicable.			
Verified Small Entity statement must also be filed			
(Note 37 CFR 1.9, 1.27, 1.28).			
SUBTOTAL			= 912.00
Processing fee of \$130. for furnishing the English			
translation later than / /20 / /30 months from the			
earliest claimed priority date (37 CFR 1.492(f)). +			
TOTAL NATIONAL FEE			= 912.00
Fee for recording the enclosed assignment (37 CFR 1.21(h)).			
The assignment must be accompanied by an appropriate cover			
sheet (37 CFR 3.28, 3.31) \$40.00 per property = 40.00			
TOTAL FEES ENCLOSED			= \$ 952.00
Amount to be			
refunded: \$			
Charged \$			

a./X/ A check in the amount of \$952. to cover the above fees is enclosed.

b./ / Please charge my Deposit Account No. \_\_\_\_\_ in the amount of \$ \_\_\_\_\_ to cover the above fees. A duplicate copy of this sheet is enclosed.

c./X/ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 11-0345. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:  
KEIL & WEINKAUF  
1101 Connecticut Ave., N.W.  
Washington, D. C. 20036Herbert B. Keil  
NAME  
18,967  
Registration No.

SIGNATURE

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the Application of )  
SEULBERGER et al. ) BOX PCT

)  
International Application )  
PCT/EP 98/ 03832 )

)  
Filed: July 23, 1998 )

)  
For: DNA SEQUENCE ENCODING A HYDROXYPHENYLPYRUVATE  
DIOXYGENASE, AND ITS OVERPRODUCTION IN PLANTS

PRELIMINARY AMENDMENT

Honorable Commissioner of  
Patents and Trademarks  
Washington, D.C. 20231

Sir:

Prior to examination, kindly amend the above-identified application as follows:

IN THE CLAIMS

Claim 12, line 2, delete "any one of claims 2 to 5" and insert --claim 2--.

Claim 16, line 1, delete "any of claims 14 and 15" and insert --claim 14--.

Delete claim 17.

22. (amended) The use of the expression cassette as claimed in claim 2 for generating plants with elevated resistance to HPPD inhibitors by means of higher expression of a DNA sequence [as claimed in claim 1] SEQ ID NO:1 and DNA sequences hydridizing therewith, encoding an HPPD.

Claim 24, lines 2 and 3, delete "any of claims 2 to 5" and insert --claim 2--.

REMARKS

The claims have been amended to eliminate multiple dependency and to put them in better form for U.S. filing. No new matter has been added.

Favorable action is solicited.

Respectfully submitted,

KEIL & WEINKAUF

Herbert B. Keil  
Reg. No. 18,967

1101 Connecticut Ave., N.W.  
Washington, D.C. 20036  
(202)659-0100

7/PRTS

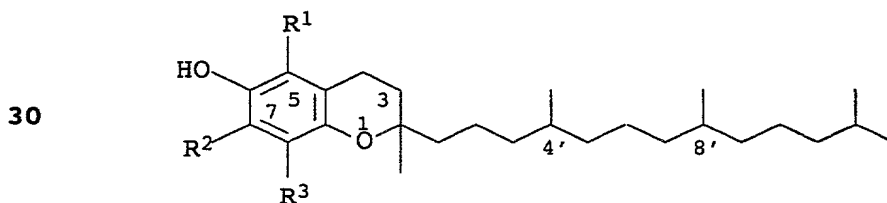
DNA sequence encoding a hydroxyphenylpyruvate dioxygenase, and its overproduction in plants

- 5 The present invention relates to a method of generating plants with an elevated vitamin E content by expressing an exogenous or endogenous HPPD gene in plants or plant organs. The invention furthermore relates to the use of the corresponding nucleic acids encoding an HPPD gene in transgenic plants to make the latter
- 10 resistant to HPPD inhibitors, and to the use of the DNA sequence encoding an HPPD for generating a test system for identifying HPPD inhibitors.

An important aim in plant molecular genetics is the generation of

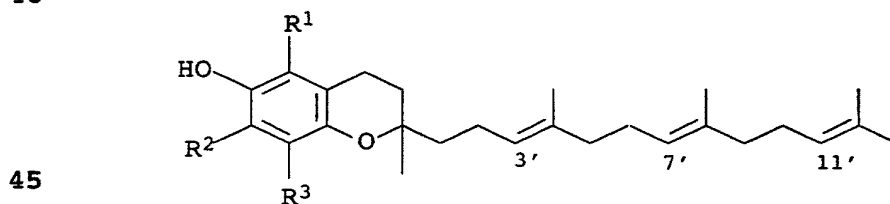
15 plants with an elevated content of sugars, enzymes and amino acids. It would also be economically interesting to develop plants with an elevated vitamin content, eg. an elevated vitamin E content.

- 20 The eight naturally occurring compounds with vitamin E activity are derivatives of 6-chromanol (Ullmann's Encyclopedia of Industrial Chemistry, Vol. A 27 (1996), VCH Verlagsgesellschaft, Chapter 4., 478-488, Vitamin E). The first group (1a - d) is derived from tocol, while the second group is composed of
- 25 tocotrienol derivatives (2a - d):



- 35 1a,  $\alpha$ -tocopherol:  $R^1 = R^2 = R^3 = \text{CH}_3$   
 1b,  $\beta$ -tocopherol [148-03-8]:  $R^1 = R^3 = \text{CH}_3$ ,  $R^2 = \text{H}$   
 1c,  $\gamma$ -tocopherol [54-28-4]:  $R^1 = \text{H}$ ,  $R^2 = R^3 = \text{CH}_3$   
 1d,  $\delta$ -tocopherol [119-13-1]:  $R^1 = R^2 = \text{H}$ ,  $R^3 = \text{CH}_3$

40



## 2

2a,  $\alpha$ -tocotrienol [1721-51-3]:  $R^1 = R^2 = R^3 = CH_3$

2b,  $\beta$ -tocotrienol [490-23-3]:  $R^1 = R^3 = CH_3$ ,  $R^2 = H$

2c,  $\gamma$ -tocotrienol [14101-61-2]:  $R^1 = H$ ,  $R^2 = R^3 = CH_3$

2d,  $\delta$ -tocotrienol [25612-59-3]:  $R^1 = R^2 = H$ ,  $R^3 = CH_3$

5

$\alpha$ -Tocopherol is of great economic importance.

The development of crop plants with an elevated vitamin E content by means of tissue culture or seed mutagenesis and natural selection has its limits. On the one hand, the vitamin E content must be detectable as early as at the tissue culture level and, on the other hand, only those plants can be manipulated via tissue culture techniques which can successfully be regenerated into entire plants, starting from cell cultures. Moreover, following mutagenesis and selection, crop plants may show undesirable characteristics which have to be eliminated by back-crossing, in some cases repeated back-crossing. Also, elevation of the vitamin E content by means of crossing would be limited to plants of the same species.

20

Those are the reasons why the genetic engineering approach, viz. isolating an essential biosynthesis gene which encodes the vitamin E synthesis performance and transferring it specifically into crop plants, is superior to the traditional breeding method. The conditions for this method are that the biosynthesis and its regulation are known and that genes which affect biosynthesis performance are identified.

25

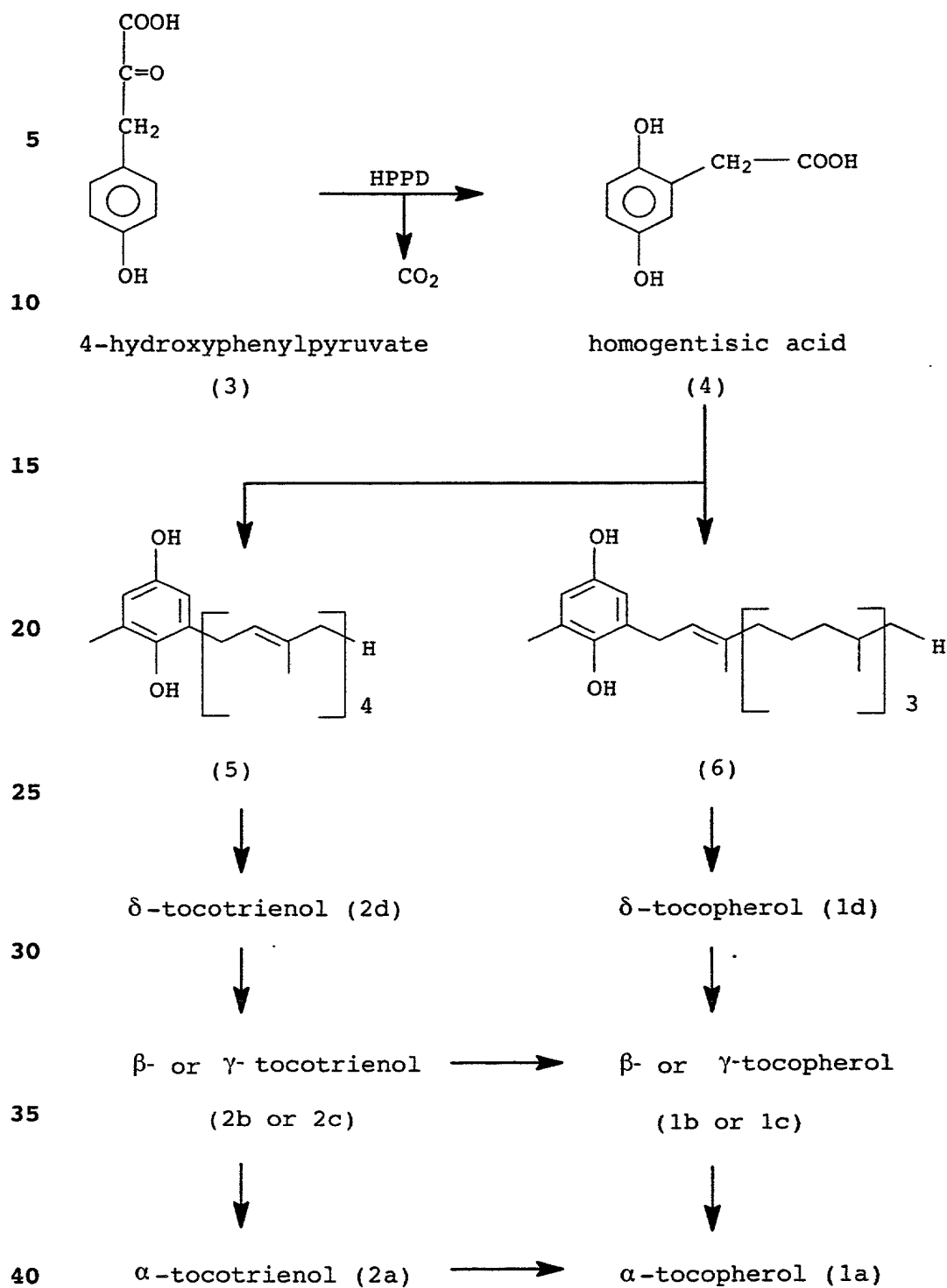
Tocopherol biosynthesis in plants and algae proceeds in a known manner and is as follows:

30

35

40

45



The precursor of the aromatic ring of the tocopherols is p-hydroxyphenylpyruvate (3), which is converted enzymatically into homogentisic acid (4) with the aid of the enzyme hydroxyphenylpyruvate dioxygenase (HPPD), and the homogentisic acid reacts with phytyl pyrophosphate with elimination of CO<sub>2</sub> to give the precursor (6). The tocotrienol biosynthesis route starts with a condensation reaction between homogentisic acid (4) and geranylgeranyl pyrophosphate to give the precursor (5). Enzymatic cyclization of the precursors 5 or 6 gives  $\delta$ -tocotrienol or  $\delta$ -tocopherol, respectively. Some of these biosynthesis enzymes have been isolated.

While searching for Arabidopsis mutants with defects in the carotenoid biosynthesis, a white phenotype mutant was identified which is not capable of producing active HPPD. If this mutant, termed *pds2*, is raised in the presence of homogentisic acid, it produces carotenoids, like the wild type, and greens (Norris et al., Plant Cell (1995) 7: 2139 - 2149). This work shows that HPPD activity is a prerequisite for the formation of photosynthetically active chloroplasts. Without this enzyme, no plastoquinones are formed, which are required as acceptors for liberated reduction equivalents during carotenoid biosynthesis (phytoene desaturation). The fact that HPPD has a key role in the plastid metabolism makes it an interesting target for herbicides. Sulcotriones efficiently inhibit the activity of the enzyme (Schultz et al., FEBS Lett. (1993) 318: 162 - 166).

Sequences of HPPD-specific genes are already known from the organisms mentioned below:

30

35

40

45

Organism	Sequence name	Access number database
Humans	HPPD_HUMAN	X72389
Pig	HPPD_PIG	D13390
Rat	HPPD_RAT	M18405
Mouse	HPPD_MOUSE	D29987
Streptomyces avermitilis	SA11864	U11864
Pseudomonas sp. strain P.J. 874	HPPD_PSESP	P80064
Arabidopsis	HPPD_ARAB1	AF900228
	HPPD_ARAB2	U89267

Furthermore, the following sequences, which show a marked homology with HPPD sequences, can be found in the databases:

PEA3\_MOUSE: Mus muscula (mouse) PEA3 polypeptide, AC X63190;

5

MELA\_SHECO: Shewanella colwelliana, mela protein, AC M59289.

WO 96/38567 describes the HPPD DNA sequence from *Arabidopsis thaliana* and *Daucus carota*.

10

A knowledge of the HPPD DNA sequences is an absolute prerequisite both for the use in crop protection for the generation of herbicide-resistant plants and for increasing the vitamin E synthesis in plants, for example for producing animal feeds with  
15 elevated vitamin E content.

It is an object of the present invention to develop a transgenic plant with elevated vitamin E content.

20 It is a further object of the present invention to develop a transgenic plant which is resistant to HPPD inhibitors.

We have found that these objects are achieved, surprisingly, by overexpressing an HPPD gene in the plants.

25

It is an additional object of the present invention to develop a test system for identifying HPPD inhibitors.

We have found that this object is achieved by expressing a barley

30 HPPD gene in a plant or in a microorganism and subsequently testing chemicals for inhibition of HPPD enzyme activity.

A first aspect of the present invention relates to the cloning of the complete barley HPPD gene via isolating the

35 HPPD-gene-specific cDNA (HvSD36).

During leaf senescence, the vitamin E content in the leaves is markedly increased (Rise et al., Plant Physiol. (1989) 89:

1028 - 1030). The monocotyledonous leaf of barley represents a

40 gradient of cells of different ages since the leaf has a basal meristem, from which new cells are formed by successive division. Thus, the oldest cells are located at the leaf tip and the youngest at the base. Fig. 1 shows a diagram of the primary leaf of barley on various days after sowing. The total leaf length

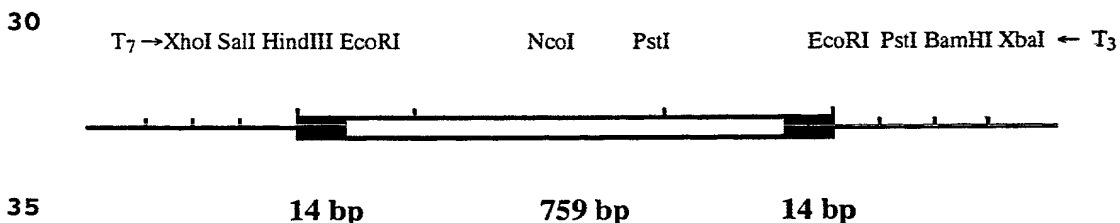
45 measured can be seen from the scale on the left-hand side. Shown, and termed I - IV, are the leaf sections of the primary leaf which are differentiated to various degrees and which have been



selected for gene expression analysis. The plants were raised in a daily light/dark photoperiod (L/D) and, for inducing senescence, were excised after 6 days and incubated for 2 days in the dark (2 nD). A "Northern blot" analysis of RNA from the barley primary leaf from sections which had differentiated to various degrees (see Fig. 2) suggest that HPPD expression in barley is controlled in a development-dependent manner. Thus, copious accumulation of the approx. 1600 nt long transcript takes place in the meristematic region on the primary leaf base (I). The content of this transcript decreases with increasing age of the tissue (IIa and IIb) and increases again in the fully differentiated cells with mature chloroplasts (III). Finally, the content of the 1600 nt long transcript is highest in the senescing sections of the primary leaf (IV). In addition, an approx. 3100 nt long transcript can be detected only in the meristematic cells on the base of the primary leaf. Again, this transcript can no longer be detected with increasing tissue maturation.

With the aid of the so-called "Differential Display" method, a 207 bp cDNA fragment was first isolated whose corresponding transcript accumulates in the primary leaf of barley in the case of dark-induced senescence. This fragment (sequence protocol: sequence ID NO:1: nucleotide position 1342 - 1549) was subsequently used as a probe to isolate a cDNA clone with a larger insert in a cDNA library (in  $\lambda$ -ZAP-II) from senescing barley flag leaves.

Diagram of the cDNA subclone HvSD 36 from the  $\lambda$ -ZAP-II library:



The cDNA fragment (sequence protocol: Sequence ID NO:1: nucleotide position 771 - 1529) was cloned into the EcoRI cleavage site of pBluescript(SK<sup>-</sup>). In addition, both ends of the cDNA are equipped with a 14 bp adaptor sequence which was required for ligation into  $\lambda$ -ZAP-II. Selected restriction sites of the vector and of the cDNA itself are shown.

45 The 759 bp long cDNA fragment was used as probe in a further experiment to obtain a complete sequence of HvSD 36. To this end, a cDNA library from RNA of the meristematic section of 5-day-old

barley seedlings was available. The lambda phage ExCell Eco RICIP from Pharmacia (Freiburg) (product number: 27-5011, 45.5kb) was used for this cDNA library.

- 5 A 1565 bp long cDNA clone was isolated, see sequence protocol: sequence ID NO:1: and 2.

Amongst the sequences in the databases, the 434 amino acids long protein sequence has a homology of 58%, which is the highest

- 10 homology with the HPPD sequence from *Arabidopsis thaliana*.

To find a genomic clone which contains the complete HPPD gene sequence, a lambda FIXII library of barley was obtained from Stratagene (Heidelberg, product number 946104). The library was  
15 prepared using DNA from etiolated leaves of winter barley cv. Igri. The DNA was subjected to partial digestion with Sau3AI. Prior to cloning into the XhoI cleavage site of the vector, the fragment ends and the phage arms were filled up with nucleotides. Screening of the library with 200,000 pfu in the first round gave  
20 only one clone which hybridized with cDNA HvSD36. After subjecting this recombinant phage to restriction digestion with PstI and SacI, fragments of a size of 5400, 3800 and 1800 bp, respectively, were isolated which can be detected in a "Southern" blot hybridization with the HvSD36 probe. These sub-fragments  
25 exist in cloned form in the Bluescript vector. Figure 3 shows the construction of the barley HPPD gene in the form of a diagram.

- The invention relates in particular to expression cassettes whose sequence encodes an HPPD or a functional equivalent thereof, and  
30 to the use of these expression cassettes for generating a plant with an elevated vitamin E content. The nucleic acid sequence may be, for example, a DNA or a cDNA sequence. Encoding sequences which are suitable for insertion into an expression cassette according to the invention are, for example, those which encode  
35 an HPPD and which impart, to the host, the ability to overproduce vitamin E.

- In addition, the expression cassettes according to the invention comprise regulatory nucleic acid sequences which govern  
40 expression of the encoding sequence in the host cell. In accordance with a preferred embodiment, an expression cassette according to the invention comprises upstream, ie. on the 5' end of the encoding sequence, a promoter and downstream, ie. on the 3' end, a polyadenylation signal and, if appropriate, other  
45 regulatory elements which are operatively linked with the encoding sequence for the HPPD gene which is located in-between. Operative linkage is to be understood as meaning the sequential

arrangement of promoter, encoding sequence, terminator and, if appropriate, other regulatory elements in such a way that each of the regulatory elements can fulfill its function as intended when the encoding sequence is expressed. The sequences preferred for operative linkage, but not limited thereto, are targeting sequences for guaranteeing subcellular localization in the apoplast, in the vacuole, in plastids, in the mitochondrion, in the endoplasmatic reticulum (ER), in the nucleus, in liposomes or in other compartments and translation enhancers such as the 5' leader sequence from the tobacco mosaic virus (Gallie et al., Nucl. Acids Res. 15 (1987) 8693 - 8711).

For example, the plant expression cassette can be incorporated into the tobacco transformation vector pBinAR-Hyg. Fig. 4 shows the tobacco transformation vectors pBinAR-Hyg with 35S promoter (A) and pBinAR-Hyg with seed-specific promoter phaseolin 796 (B):

- HPT: hygromycin phosphotransferase
  - OCS: octopine synthase terminator
  - PNOS: nopaline synthase promoter
  - those restriction sites which cleave the vector only once are also shown.
- Suitable as promoters of the expression cassette according to the invention are, in principle, all promoters which can control the expression of foreign genes in plants. In particular a plant promoter or a promoter derived from a plant virus is preferably used. Particularly preferred is the CaMV 35S promoter from cauliflower mosaic virus (Franck et al., Cell 21 (1980) 285 - 294). It is known that this promoter contains various recognition sequences for transcriptional effectors which in their entirety lead to permanent and constitutive expression of the gene introduced (Benfey et al., EMBO J. 8 (1989) 2195 - 2202).
- The expression cassette according to the invention may additionally comprise a chemically inducible promoter by means of which expression of the exogenous HPPD gene in the plant can be controlled at a specific point in time. Such promoters which can be used are, inter alia, for example the PRP1 promoter (Ward et al., Plant. Mol. Biol. 22 (1993), 361-366), a promoter which can be induced by salicylic acid (WO 95/19443), a promoter which can be induced by benzenesulfonamide (EP-A 388186), a promoter which can be induced by tetracyclin (Gatz et al., (1992) Plant J. 2, 397-404), a promoter which can be induced by abscisic acid

(EP-A 335528) or a promoter which can be induced by ethanol or cyclohexanone (WO 93/21334).

Furthermore, particularly preferred promoters are those which  
5 ensure expression in tissues or plant organs in which the biosynthesis of vitamin E, or its precursors, takes place. Promoters which must be mentioned in particular are those which guarantee leaf-specific expression. Promoters which may be mentioned are the potato cytosolic FBPase or the potato ST-LSI  
10 promoter (Stockhaus et al., EMBO J. 8 (1989) 2445 - 245).

With the aid of a seed-specific promoter, it was possible stably to express a foreign protein in the seeds of transgenic tobacco plants in an amount of up to 0.67% of the total soluble seed  
15 protein (Fiedler and Conrad, Bio/Technology 10 (1995), 1090-1094). The expression cassette according to the invention can therefore contain, for example, a seed-specific promoter (preferably the phaseolin promoter (US 5504200), the USP (Baumlein, H. et al. Mol. Gen. Genet. (1991) 225 (3), 459 - 467)  
20 or LEB4 promoter (Fiedler and Conrad, 1995)), the LEB4 signal peptide, the gene to be expressed and an ER retention signal. The construction of such a cassette is shown in the form of a diagram in Figure 4 by way of example.

25 An expression cassette according to the invention is prepared by fusing a suitable promoter with a suitable HPPD DNA sequence and preferably a DNA which is inserted between promoter and HPPD DNA sequence and which encodes a chloroplast-specific transit peptide, and a polyadenylation signal, using customary  
30 recombination and cloning techniques as they are described, for example, in T. Maniatis, E.F. Fritsch and J. Sambrook, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989) and in T.J. Silhavy, M.L. Berman and L.W. Enquist, Experiments with Gene Fusions, Cold Spring Harbor  
35 Laboratory, Cold Spring Harbor, NY (1984) and in Ausubel, F.M. et al., Current Protocols in Molecular Biology, Greene Publishing Assoc. and Wiley-Interscience (1987).

Particularly preferred sequences are those which guarantee  
40 targeting into the apoplast, into plastids, into the vacuole, the mitochondrion, the endoplasmatic reticulum (ER), or, by means of the absence of suitable operative sequences, the remaining in the compartment of formation, the cytosol (Kermode, Crit. Rev. Plant Sci. 15, 4 (1996), 285 - 423). Localization in the ER has proved  
45 to be especially advantageous for the amount of protein

accumulation in transgenic plants (Schouten et al. , Plant Mol. Biol. 30 (1996), 781 - 792).

The invention also relates to expression cassettes whose DNA  
5 sequence encodes an HPPD fusion protein, a moiety of the fusion  
protein being a transit peptide which governs translocation of  
the polypeptide. Especially preferred are chloroplast-specific  
transit peptides which are cleaved enzymatically from the HPPD  
moiety after the HPPD gene product has been translocated into the  
10 chloroplasts. Particularly preferred is the transit peptide which  
is derived from plastid transketolase (TK) or a functional  
equivalent of this transit peptide (eg. the transit peptide of  
the small subunit of rubisco or of Ferredoxin NADP  
oxidoreductase).

15 The HPPD-encoding nucleotide sequence inserted can be prepared  
synthetically or obtained naturally or comprise a mixture of  
synthetic and natural DNA components. In general, there are  
prepared synthetic nucleotide sequences with codons which are  
20 preferred by plants. These codons which are preferred by plants  
can be determined from amongst codons with the highest protein  
frequency which are expressed in most interesting plant species.  
When preparing an expression cassette, various DNA fragments may  
be manipulated in order to obtain a nucleotide sequence which  
25 expediently reads in the correct direction and which is provided  
with a correct reading frame. To connect the DNA fragments to  
each other, adaptors or linkers may be joined onto the fragments.

The promoter and terminator regions according to the invention  
30 may advantageously be provided, in the direction of  
transcription, with a linker or polylinker which comprises one or  
more restriction sites for insertion of this sequence. As a rule,  
the linker has 1 to 10, in most cases 1 to 8, preferably 2 to 6,  
restriction sites. In general, the linker within the regulatory  
35 regions has a size of less than 100 bp, frequently less than  
60 bp, but at least 5 bp. The promoter according to the invention  
may be both native, or homologous, but also foreign, or  
heterologous, to the host plant. The expression cassette  
according to the invention comprises, in the 5'-3' transcription  
40 direction, the promoter according to the invention, any desired  
DNA sequence and a region for transcriptional termination.  
Various termination regions can be exchanged for each other as  
desired.

45 It is furthermore possible to employ manipulations which provide  
suitable restriction sites or which remove excess DNA or  
restriction sites. Where insertions, deletions or substitutions,

eg. transitions and transversions, are suitable, it is possible to use *in vitro* mutagenesis, primer repair, restriction or ligation. In the case of suitable manipulations, eg. restriction, chewing back or filling up overlaps for blunt ends, complementary 5 ends of the fragments may be provided for ligation.

What may be of importance for the success according to the invention is, inter alia, attaching the specific ER retention signal SEKDEL (Schouten, A. et al. Plant Mol. Biol. 30 (1996), 10 781 - 792), which results in a three to four times higher than average expression level. Other retention signals which occur naturally in plant and animal proteins which are localized in the ER may also be used for constructing the cassette.

15 Preferred polyadenylation signals are plant polyadenylation signals, preferably those which correspond essentially to T-DNA polyadenylation signals from *Agrobacterium tumefaciens*, in particular of gene 3 of the T-DNA (octopine synthase) of the Ti plasmid pTiACH5 (Gielen et al., EMBO J. 3 (1984) 835 et seq.), or 20 functional equivalents.

An expression cassette according to the invention may comprise, for example, a constitutive promoter (preferably the CaMV 35S promoter), the LeB4 signal peptide, the gene to be expressed and 25 the ER retention signal. The preferred ER retention signal used is the amino acid sequence KDEL (lysine, aspartic acid, glutamic acid, leucine).

The fused expression cassette which encodes an HPPD gene is 30 preferably cloned into a vector, for example pBin19, which is suitable for transforming *Agrobacterium tumefaciens*. *Agrobacteria* which are transformed with such a vector can then be used in the known manner for transforming plants, in particular crop plants, eg. tobacco plants, for example by immersing scarified leaves or 35 leaf sections in an *agrobacteria* solution and subsequently growing them in suitable media. The transformation of plants by means of *agrobacteria* is known, inter alia, from F.F. White, Vectors for Gene Transfer in Higher Plants; in Transgenic Plants, Vol. 1, Engineering and Utilization, Eds. S.D. Kung and R. Wu, 40 Academic Press, 1993, pp. 15 - 38. The transformed cells of the scarified leaves or leaf sections can be used for regenerating, in the known manner, transgenic plants which contain a gene for expression of an HPPD gene integrated into the expression cassette according to the invention.

- To transform a host plant with an HPPD-encoding DNA, an expression cassette according to the invention is incorporated into a recombinant vector in the form of an insertion, and the vector DNA of this recombinant vector additionally comprises
- 5 functional regulation signals, for example sequences for replication or integration. Suitable vectors are described, inter alia, in "Methods in Plant Molecular Biology and Biotechnology" (CRC Press), Chapter. 6/7, pp. 71 - 119 (1993).
- 10 Using the above-cited recombination and cloning techniques, the expression cassettes according to the invention can be cloned into suitable vectors which allow their multiplication, for example in *E. coli*. Suitable cloning vectors are, inter alia, pBR332, pUC series, M13mp series and pACYC184. Especially
- 15 suitable are binary vectors which are capable of replicating not only in *E. coli*, but also in agrobacteria.

- The invention furthermore relates to the use of an expression cassette according to the invention for transforming plants,
- 20 plant cells, plant tissues or plant organs. The preferred purpose of the use is to raise the vitamin E content of the plant.

- Depending on the choice of the promoter, expression may take place specifically in the leaves, in the seeds or in other plant
- 25 organs. The present invention also relates to such transgenic plants, their propagation material and their plant cells, plant tissues or plant organs.

- In addition, the expression cassette according to the invention
- 30 may also be employed for transforming bacteria, cyanobacteria, yeasts, filamentous fungi and algae with the purpose of raising the vitamin E production.

- The transfer of foreign genes into the genome of a plant is
- 35 termed transformation. This process exploits the previously described methods of transforming and regenerating plants from plant tissues or plant cells to obtain transient or stable transformation. Suitable methods are protoplast transformation by polyethylene-glycol induced DNA uptake, the ballistic method with
- 40 the gene gun - the so-called particle bombardment method, electroporation, incubation of dry embryos in DNA-containing solution, microinjection and *Agrobacterium*-mediated gene transfer. The abovementioned methods are described, for example, in B. Jenes et al., Techniques for Gene Transfer, in: Transgenic
- 45 Plants, Vol. 1, Engineering and Utilization, Eds. S.D. Kung and R. Wu, Academic Press (1993) 128 - 143, and in Potrykus Annu. Rev. Plant Physiol. Plant Molec. Biol. 42 (1991) 205 - 225). The

construct to be expressed is preferably cloned into a vector which is suitable for transforming *Agrobacterium tumefaciens*, for example pBin19 (Bevan et al., Nucl. Acids Res. 12 (1984) 8711).

- 5 *Agrobacteria* transformed with an expression cassette according to the invention can also be used, in a known manner, for transforming of plants, in particular crop plants such as cereals, maize, oats, soya, rice, cotton, sugar beet, canola, sunflowers, flax, hemp, potatoes, tobacco, tomatoes, oilseed
- 10 rape, alfalfa, lettuce and the various tree, nut and grapevine species, for example by immersing scarified leaves or leaf sections in an *agrobacteria* solution and subsequently growing them in suitable media.
- 15 Functionally equivalent sequences which encode an HPPD gene are, in accordance with the invention, those sequences which still have the desired functions despite a different nucleotide sequence. Thus, functional equivalents embrace naturally occurring variants of the sequences described herein and also
- 20 artificial nucleotide sequences, eg. artificial nucleotide sequences which have been obtained by chemical synthesis and which are adapted to the codon usage of a plant.

- A functional equivalent is also to be understood as meaning, in
- 25 particular, natural or artificial mutations of an originally isolated HPPD-encoding sequence which continues to show the desired function. Mutations encompass substitutions, additions, deletions, inversions or insertions of one or more nucleotide residues. Thus, the present invention also encompasses those
- 30 nucleotide sequences which are obtained by modifying the present nucleotide sequence. The purpose of such a modification may be, for example, a further limitation of the encoding sequence contained therein, or else, for example, the insertion of further cleavage sites for restriction enzymes.

- 35 Functional equivalents are also those variants whose function is less or more pronounced in comparison with the starting gene or gene fragment.

- 40 Also suitable are artificial DNA sequences as long as they, as described above, mediate the desired characteristic of raising the vitamin E content in the plant by overexpressing the HPPD gene in crop plants. Such artificial DNA sequences can be determined for example by back-translation of proteins
- 45 constructed with the aid of molecular modeling and which have HPPD activity, or by *in vitro* selection. Especially suitable are encoding DNA sequences which were obtained by back-translating a



polypeptide sequence in accordance with the codon usage specific to the host plant. The specific codon usage can be determined readily by an expert familiar with plant genetic methods using computer evaluations of other, known genes of the plant to be  
5 transformed.

Further suitable equivalent nucleic acid sequences according to the invention which must be mentioned are sequences which encode fusion proteins, a component of the fusion protein being a plant  
10 HPPD polypeptide or a functionally equivalent moiety thereof. The second moiety of the fusion protein can be, for example, a further polypeptide with enzymatic activity or an antigenic polypeptide sequence with the aid of which the detection of HPPD expression is possible (eg. myc-tag or his-tag). However, this is  
15 preferably a regulatory protein sequence, eg. a signal or transit peptide, which leads the HPPD protein to the desired site of action.

However, the invention also relates to the expression products  
20 and fusion products, of a transit peptide and a polypeptide with HPPD activity, which have been produced in accordance with the invention.

Raising the vitamin E content means, for the purposes of the  
25 present invention, the artificially acquired ability of an elevated vitamin E biosynthesis performance by means of functional overexpression of the HPPD gene in the plant in contrast to the non-genetically-engineered plant for the duration of at least one plant generation.

30 The vitamin E biosynthesis site is generally the leaf tissue, so that leaf-specific expression of the HPPD gene is expedient. However, it will be understood readily that vitamin E biosynthesis is not necessarily restricted to the leaf tissue,  
35 but may also take place tissue-specifically in all other organs of the plant, for example in fatty seeds.

In addition, constitutive expression of the exogenous HPPD gene is advantageous. On the other hand, inducible expression may also  
40 appear desirable.

The efficacy of expression of the transgenically expressed HPPD gene can be determined for example *in vitro* by shoot meristem propagation. In addition, changes in the nature and level of HPPD  
45 gene expression, and its effect on the vitamin E biosynthesis

15

performance on test plants, can be tested in greenhouse experiments.

The invention furthermore relates to transgenic plants  
5 transformed with an expression cassette according to the invention, and to transgenic cells, tissues, organs and propagation material of such plants. Especially preferred in this context are transgenic crop plants, eg. barley, wheat, rye, maize, oats, soya, rice, cotton, sugar beet, canola, sunflowers,  
10 flax, hemp, potatoes, tobacco, tomatoes, oilseed rape, alfalfa, lettuce and the various tree, nut and grapevine species.

Plants for the purposes of the invention are mono- and dicotyledonous plants or algae.

15

As already mentioned, HPPD is a suitable target for sulcotrione-type herbicides. To allow even more efficient HPPD inhibitors, it is necessary to provide suitable test systems with which inhibitor/enzyme binding studies can be carried out. To  
20 this end, for example, the complete barley HPPD cDNA sequence is cloned into an expression vector (pQE, Qiagen) and overexpressed in *E. coli*.

The HPPD protein expressed with the aid of the expression  
25 cassette according to the invention is particularly suitable for finding HPPD-specific inhibitors.

To this end, the HPPD can be employed, for example, in an enzyme assay in which the HPPD activity is determined in the presence  
30 and absence of the active substance to be tested. A comparison of the two activity determinations allows qualitative and quantitative findings on the inhibitory behavior of the active substance to be tested to be obtained.

35 The test system according to the invention allows a large number of chemical compounds to be screened rapidly and simply for herbicidal properties. The method allows the targeted and reproducible selection, amongst a large number of substances, of those with great potency in order to subject these substances  
40 subsequently to further in-depth tests with which the expert is familiar.

The invention furthermore relates to herbicides which can be identified with the above-described test system.

45

## 16

Overexpression in a plant of the gene sequence Seq ID NO: 1, which encodes an HPPD, results in an elevated resistance to HPPD inhibitors. The invention also relates to the transgenic plants thus generated.

5

The invention furthermore relates to:

- A method of transforming a plant, which comprises introducing an expression cassette according to the invention into a plant cell, into callus tissue, into an entire plant or into plant protoplasts.
- The use of a plant for generating plant HPPD.
- 15 - The use of the expression cassette according to the invention for generating plants with elevated resistance to HPPD inhibitors by means of higher expression of a DNA sequence according to the invention.
- 20 - The use of the expression cassette according to the invention for generating plants with an elevated vitamin E content by means of expressing, in plants, a DNA sequence according to the invention.
- 25 - The use of the expression cassette according to the invention for generating a test system for identifying HPPD inhibitors.

The invention is illustrated by the examples which follow, but not limited thereto:

30

35

40

45

## General cloning methods

The cloning steps carried out within the scope of the present invention, eg. restriction cleavages, agarose gel electrophoresis, purification of DNA fragments, transfer of nucleic acids onto nitrocellulose and nylon membranes, linking DNA fragments, transformation of *E. coli* cells, growing bacteria, multiplying phages and sequence analysis of recombinant DNA, were carried out as described by Sambrook et al. (1989) Cold Spring Harbor Laboratory Press; ISBN 0-87969-309-6).

The bacterial strains used hereinbelow (*E. coli*, XL-I Blue) were obtained from Stratagene and, in the case of NP66, Pharmacia. The agrobacterial strain used for the transformation of plants (*Agrobacterium tumefaciens*, C58C1 with plasmid pGV2260 or pGV3850kann) was described by Deblaere et al. in (Nucl. Acids Res. 13 (1985) 4777). Alternatively, the agrobacterial strain LBA4404 (Clontech) or other suitable strains may also be employed. Vectors which can be used for cloning are the vectors pUC19 (Yanish-Perron, Gene 33 (1985), 103 - 119) pBluescript SK- (Stratagene), pGEM-T (Promega), pZerO (Invitrogen), pBin19 (Bevan et al., Nucl. Acids Res. 12 (1984), 8711 - 8720) and pBinAR (Höfgen and Willmitzer, Plant Science 66 (1990) 221 - 230).

25 Sequence analysis of recombinant DNA

Recombinant DNA molecules were sequenced using a laser fluorescence DNA sequencer by Licor (available from MWG Biotech, Ebersbach) following the method of Sanger (Sanger et al., Proc. Natl. Acad. Sci. USA 74 (1977), 5463 - 5467).

## Generation of plant expression cassettes

35 Into plasmid pBin19 (Bevan et al., Nucl. Acids Res. (1984) 12, 8711) there was inserted a 35S CaMV promoter in the form of an EcoRI-KpnI fragment corresponding to nucleotides 6909 - 7437 of cauliflower mosaic virus (Franck et al. Cell 21 (1980) 285). The polyadenylation signal of gene 3 of the T-DNA of the Ti plasmid pTiACH5 (Gielen et al., EMBO J. 3 (1984) 835), nucleotides 11749 - 11939, was isolated as a PvuII-HindIII fragment and, after addition of SphI linkers, cloned into the PvuII cleavage site between the SphI-HindIII cleavage site of the vector pBmAR-Hyg. This gave the plasmid pBinAR (Höfgen and Willmitzer, Plant Science 66 (1990) 221 - 230).

## Use Examples

## Example 1

## 5 Isolation of HPPD-specific cDNA sequences

The composition of the mRNA population from primary leaves of nine-day-old barley plants which had been grown in an L/D photoperiod (16 hours light/8 hours dark) was compared with that of primary leaves of 11-day-old barley plants in which, after a raising period of nine days, senescence was subsequently induced by a two-day dark treatment (Humbeck and Krupinska, J. Photochem. Photobiol. 36 (1996), 321 - 326) with the aid of the DDRT-PCR method published by Liang and Pardee (Science (1992) 257, 967 - 972). In each case 0.2 µg of the total RNA was converted into cDNA using the enzyme "Superscript RT" (Gibco BRL, Eggenstein). In addition to the RNA, the reaction batches (20 µl) also contained 20 µM dNTPs, 10 µM DTT, 1xRT buffer and in each case 1 µM (dT)<sub>12</sub>VN primer. The anchor "primers" required for these reactions were synthesized on the basis of the data of Liang and Pardee:

1. 5'-TTTTTTTTTTTTTAG-3'
2. 5'-TTTTTTTTTTTTTCA-3'
- 25 3. 5'-TTTTTTTTTTTTTAC-3'
4. 5'-TTTTTTTTTTTTTGT-3'

After the cDNAs were synthesized, amplification of the relevant sequences was effected in each case in ten batches, which differ by the use of the random "primers" given hereinbelow:

- |                        |                      |
|------------------------|----------------------|
| 1. 5'-TACAACGAGG-3'    | 2. 5'-GGAACCAATC-3'  |
| 3. 5'-AAACTCCGTC-3'    | 4. 5'-TGGTAAAGGG-3'  |
| 5. 5'-CTGCTTGATG-3'    | 6. 5'-GTTTTCGCAG-3'  |
| 35 7. 5'-GATCTCAGAC-3' | 8. 5'-GATCTAACCG-3'  |
| 9. 5'-GATCATGGTC-3'    | 10. 5'-GATCTAAGGC-3' |

In a volume of in each case 20 µl, the PCR reaction batches contained 1xPCR buffer, 2 µM dNTPs, 2.5 µCi (α <sup>33</sup>P)-dATP, 1 µM (dT)<sub>12</sub>VN-"primer", 1/10 vol. RT mix (Sambrook et al. Molecular Cloning - A Laboratory Manual, 1989), 1 U Taq DNA polymerase (Boehringer, Mannheim) and 1 µM 10-mer random "primers". The PCR-reactions proceeded in a Uno block (Biometra) following the program below:

- 45 1. 94°C 2 min
2. 94°C 30 s

3. 40°C 2 min
4. 72°C 30 s
5. 72°C 5 min
6. 4°C storage until further processing

5

Steps 2, 3 and 4 were carried out 40 times in succession. This gave approximately 100 cDNA bands per reaction and "primer" combination.

- 10 In contrast to the protocol of Liang and Pardee, the amplified cDNA fragments were separated in non-denaturing polyacrylamide gels of the following composition: 6% (w/v) acrylamide (Long Ranger, AT Biochem), 1.2 x TBE buffer, 0.005% (v/v) TEMED and 0.005% (w/v) APS (Bauer et al, Nucl. Ac. Res. (1993) 21, 15 4272 - 4280).

- In each case 3.5 µl of each PCR batch were treated with 2 µl of loading buffer (dye II, Sambrook et al., 1989) and then loaded onto the gel. To determine the reproducibility of the cDNA band patterns (Fig. 5), in each case two independent RNA preparations (9 and 9', 11 and 11') were prepared from the barley primary leaves harvested on days 9 and 11 and used in parallel in the analysis below. What is shown is the result of two different primer combinations (A and B); by way of example, two differences in the band pattern between the sample of days 9 and 11 were emphasized by arrows. Only those bands which occurred equally in the two samples from senescing plants and which did not occur in the two comparison samples were taken into consideration when analyzing the gels at a later point in time. Electrophoresis was carried out over a period of 2.5 hours at 40 watt (0.8 w/cm<sup>3</sup>) in 1 x TBE buffer. After separation of the cDNA fragments had occurred, the gel was transferred onto filter paper (Schleicher & Schüll, Dassel). After the gel had been dried at 50°C, an X-ray film was placed on top of it. cDNA bands which were only found in the case of samples 11 and 11' in the autoradiograph were excised from the dry gel using a surgical blade, and the DNA was eluted by boiling in 100 µl 1 x TE buffer. The ethanol-precipitated DNA was resuspended in 10 µl of water for further tests. After reamplification with the "primers" previously used for this batch, the DNA was cloned and sequenced and also employed as a probe for Northern blot hybridizations.

- To test if the relevant cDNA fragment actually represents a senescence-specifically occurring transcript, hybridizations were carried out with RNA from leaves of various developmental stages:

## 20

- A. 1. RNA from primary leaves from plants raised for 9 days in an L/D photoperiod
- A. 3. RNA from primary leaves from 10-day-old plants raised without a light phase on day 10
- A. 4 RNA from primary leaves from 11-day-old plants which lacked a light phase on days 10 and 11
- 10 A. 5 RNA from primary leaves from 12-day-old plants which underwent a further light phase after 2 days in the dark

The samples for RNA analysis were harvested in each case in the middle of the original night phase.

- 15 B. RNA from flag leaves which had been collected in the field at seven different points in time (Fig. 6). The leaves were fully grown on 29 May and showed less than 10% of the original chlorophyll content on 21 June. The beginning of the senescence processes is shown in Figure 6 by an arrow (ie. 17 days after reaching the full length on 15 June). The beginning of senescence was defined as the day on which photosystem II efficacy dropped (Humbeck et al., Plant Cell Environment (1996) 19: 337 - 344).

To hybridize a filter with the above-described RNA samples, a specific probe for the *rbcS* gene, which encodes the small sub-unit of ribulose-1,5-bisphosphate carboxylase, was also employed in addition to the HPPD probe, for comparison reasons. Figure 6 shows hybridization of the "Northern blots" A and B with cDNA HvSD36 and with a probe which is specific for the *rbcS* gene. Filter A carries RNA from barley primary leaves after a raising period of 9 days in an L/D photoperiod (9), after subsequent incubation in the dark for one and two days, respectively (10, 11) and after subsequent return to light conditions for one day (12). Filter B contains RNA from flag leaves which had been harvested in the field in the period from 29.05. to 21.06.1992. The arrow indicates the beginning of senescence on 15.06. As can be seen from Figure 6, the amount of *rbcS*-specific mRNA is high when the amount of HPPD-specific mRNA is relatively low. In primary leaves of nine-day-old plants, the HPPD-specific mRNA is not detectable prior to transfer into the dark and accumulates markedly during the dark phase. When the plants are returned to light conditions, the amount of this mRNA drops markedly. In the case of the flag leaves, small amounts of the HPPD-specific mRNA can already be detected in fully-grown, non-senescent leaves. As

early as 4 days prior to the actual beginning of senescence, expression levels are higher. The highest amount of this mRNA can be found in senescent leaves. A size comparison with known RNA species showed that the transcript detected with the cDNA probe

5 HvSD36 (s: senescence; d: dark, fragment number 36 in the DDRT gel) has a length of approx. 1.6 kb.

By means of DDRT PCR, three cDNA fragments were obtained independently of each other which showed this expression pattern

10 and which, on the basis of sequence analysis, actually represent the same transcript. The longest fragment had a size of 230 bp. The 230 bp long PCR product was finally cloned into the SmaI cleavage site of vector pUC18 using the "Sure Clone™ ligation kit" (Pharmacia, Freiburg) following the manufacturer's

15 instructions. The recombinant plasmid was transformed into competent cells of E. coli strain DH5 α. Since, for methodology reasons, the fragment represents the 3' end of the relevant transcript, the sequence information was first insufficient to identify an unambiguous homology with a sequence in the

20 databases. To isolate a longer corresponding cDNA, a lambda ZAPII library (Stratagene, Heidelberg) of RNA of senescent flag leaves was screened using the 230 bp long fragment as the probe. For this step, the probe was labeled with Dig-dUTP following the instructions of the "DNA Labeling and Detection Kit" (Boehringer,

25 Mannheim). The library was examined following the protocol of the "ZAP-cDNA Synthesis Kit" (Stratagene, Heidelberg).

In the case of the probe described herein, 150,000 pfu were examined. Of these, 39 phage plaques gave a positive signal. Of

30 these, further work was carried out on 12 phage populations. Following phage preparation, the fragments inserted were enriched via PCR and separated by electrophoresis. Southern blot hybridization with the HvSD36 probe allowed those phage populations which had the largest "inserts" with positive signal

35 to be selected amongst the 12 phage populations thus treated. After replating, the phages were subjected to a further hybridization step. Single phage plaques were excised and, after elution, subjected to an *in vivo* excision using a helper phage and following the protocol from Stratagene (Exassist™

40 Interference-Resistant Helper Phage with SOLR™ Strain). The so-called "phagemids" obtained from this treatment contain the cDNA cloned in pBLuescript (SK-).

Following a subsequent plasmid preparation, the relevant "insert"

45 was excised from the Bluescript plasmid using EcoRI. The cDNA clone obtained in the case of HvSD36 contains an "insert" with a length of approx. 800 bp. Complete sequencing of the cDNA was



carried out using the "SequiTherm Excel Long-Read DNA-Sequenzierungs-Kit" (Epicentre Technologies, Biozym Diagnostic, Oldendorf) using IRD41-labeled universal "primers" which bind to sequence regions in the Bluescript vector.

- 5 Detection of the DNA fragments was effected via the infrared laser of the automatic sequencer 4000L by Licor. After sequencing, an exactly 759 bp long sequence was present whose sides are flanked by an in each case 14 bp long adaptor sequence. These adaptor sequences were used for ligating the cDNA fragments
- 10 with the arms of phage lambda ZAPII (Stratagene, Heidelberg) when generating the c-DNA library.

- Amongst the sequences in the databases, the protein sequence HvSD36, which has a total of over 180 amino acids, has a homology
- 15 of 41% with the sequence of human HPPD which is the highest. Taking into consideration the length of the transcript detected in the "Northern blot" (approx. 1600 nt), it can be assumed that 850-900 bp are still missing from the cDNA.

- 20 To complete the cDNA, a further cDNA library was investigated. mRNA was isolated from the basal meristematic zone of 5-day-old barley seedlings with the aid of "Dynabeads" (Dynal, Hamburg) and transcribed into cDNA using the "Time Saver cDNA SyntheseKit" (Pharmacia, Freiburg). This was followed by ligation of
- 25 EcoRI/NotI adaptors (Pharmacia, Freiburg) to the cDNA with subsequent ligation into the lambda ExCell vector (Pharmacia, Freiburg). Finally, the recombinant phage DNA was packaged into phage proteins with the aid of "Gigapack II Gold Set" (Stratagene, Heidelberg). Using the 759 bp long probe HvSD36, 400,000 pfu were
- 30 screened, and 5 phages were detected by the probe. Excision of the "phagemids" from the phage was effected *in vivo* with the aid of bacterial strain NP66 following the instructions of Pharmacia (Freiburg). The recombinant pExCell plasmids were isolated from the individual bacterial colonies and transferred into bacterial
- 35 strain D115  $\alpha$  for propagation.

The longest cDNA clone HvSD36 isolated in this manner has a length of 1565 bp and was sequenced completely (see sequence protocol).

40

#### Example 2

#### Characterization of the genomic sequence

- 45 To identify a genomic clone which contains the gene sequence of HPPD, a lambda FIXII library of barley was obtained from Stratagene (Heidelberg). The library was prepared using DNA from

## 23

- etiolated leaves of winter barley cv. Igri. The DNA was partially digested with Sau3AI. Prior to cloning into the XhoI cleavage site of the vector, the fragment ends and the phage arms were filled up with nucleotides. Screening of the library with
- 5 200,000 pfu in the first round only gave one clone which hybridized with cDNA HvSD36. After subjecting this recombinant phage to restriction digestion with PstI and SacI, fragments 5400, 3800 and 1800 bp in length were subsequently isolated which can be detected with the HvSD36 probe when carrying out a
- 10 "Southern" blot hybridization. These sub-fragments exist in cloned form in the Bluescript vector.

- The library was screened following the protocol given for the HybondN membrane. Labeling of the probe for screening the library
- 15 and for the "Southern" blot hybridizations was effected via "random priming" with  $^{32}\text{P}$ -dATP using the Klenow enzyme (Sambrook et al., (1989) Molecular cloning. A laboratory manual. Cold Spring Harbor Laboratory, New York).
- 20 A genomic "Southern blot" was carried out with total DNA from barley (Carina) (Fig. 7). In each case 15  $\mu\text{g}$  of DNA were digested with BamHI (B), EcoRI (E), HindIII (H) or XbaI (X) and separated in a 0.75% agarose gel. After transfer to a Hybond N+ membrane (Amersham, Braunschweig), hybridization was effected with the
- 25 incomplete, 759 bp long cDNA probe from HvSD36 following instructions of the membrane manufacturer. The following fragments were detected:

- |           |                           |
|-----------|---------------------------|
| BamHI:    | 6.0, 3.9 and 3.0 kbp      |
| 30 EcoRI: | >10 kbp                   |
| HindIII:  | 8.3, 2.6, 1.1 and 1.0 kbp |
| XbaI:     | 9.0, 5.2 and 4.2 kbp      |

- The fragment lengths were estimated by comparison with a DNA size
- 35 standard (Kb-Leiter, GibcoBRL, Eggenstein).

## Example 3

- Homology comparison of the HvSD36 protein sequence
- 40 A comparison of the HvSD36 protein sequence with protein sequences in the database revealed homologies to the following protein sequences known to date:

		10	20	30	40	50
5	HPPD_Hv	.....	.....	.....	.....MP	PTPTTPAATG
	HPPD_Ath	.....	.....	.....	...MGHQNA	VSENQNHDDG
	HPPD_HUMAN	.....	.....	.....	.....	.....
	HPPD_RAT	.....	.....	.....	.....	.....
	HPPD_PIG	.....	.....	.....	.....	.....
	HPPD_MOUSE	.....	.....	.....	.....	.....
	HPPD_PSESP	.....	.....	.....	.....	.....
10	MELA_SHECO	.....	.....	.....	.....	.....
	PEA3_MOUSE	MTKSSNHNCL	LRPENKPLW	GPGAQAASLR	PSPATLVVSS	PGHAEHPPAA
		60	70	80	90	100
15	HPPD_Hv	AAAAVTPEHA	RPHRMVRFNP	RSDRFHTLSF	HHVEFWCADA	ASAAGRFAFA
	HPPD_Ath	AASSPGFKLV	GFSKFVRKNP	KSDKFKVKRF	HHIEFWCGDA	TNVARRFSWG
	HPPD_HUMAN	M	TTYSKDGAKP	ERGRFLH--F	HSVTFWVGNA	KQAASFYCSK
	HPPD_RAT		YWDKGP KP	ERGRFLH--F	HSVTFWVGNA	KQAASFYCNK
	HPPD_PIG	M	TSYSDKGEKP	ERGRFLH--F	HSVTFWVGNA	KQAASYYCSK
	HPPD_MOUSE	M	TTYNNKGPKP	ERGRFLH--F	HSVTFWVGNA	KQAASFYCNK
	HPPD_PSESP			ADLYENP	MGLMGFEFIE	LASPTPNTLE
	MELA_SHECO			MASEQNP	LGLLGIEFTE	FATPDLDFMH
20	PEA3_MOUSE	PAQTPGPQVS	ASARGPGPVA	GGSGRMERRM	KGGYL---DQ	RVPYTFCSSK
		110	120	130	140	150
25	HPPD_Hv	LGAPLAARSD	LSTGNSAHAS	QLLRSGSLAF	LFT--APYAN	G-CDAA----
	HPPD_Ath	LGMRFSAKSD	LSTGNMVHAS	YLLTSGDLRF	LFT--APYSP	S-LSAGEIKP
	HPPD_HUMAN	MGFEPLAYRG	LETGSREVV	HVIKQKIVF	VLS--SA---	-----LNP
	HPPD_RAT	MGFEPLAYKG	LETGSREVV	HVIKQKIVF	VLC--SA---	-----LNP
	HPPD_PIG	IGFEPLAYKG	LETGSREVV	HVVKQDKIVF	VFS--SA---	-----LNP
	HPPD_MOUSE	MGFEPLAYRG	LETGSREVV	HVIKRGKIVF	VLC--SA---	-----LNP
	HPPD_PSESP	PIFEIMGFTK	VATHRSKDV-	HLYRQGAINL	ILN--NE---	-----
	MELA_SHECO	KVFIDFGFSK	LKKHKQKDI-	VYYKQNDINF	LLN--NE---	-----
30	PEA3_MOUSE	PGNGSLGEAL	MVPQKLM DP	GSLPPSDSED	LFQDLSHFQE	TWLAEAQVPD
		160	170	180	190	200
35	HPPD_Hv	--TASLPSFS	ADAARRFSAD	HGIAVR SVAL	RVADAAEAFR	ASRRRGARPA
	HPPD_Ath	TTTASIPSF	HGSCRSFFSS	HGLGVRVAI	EVEDAESAFS	ISVANGAIPS
	HPPD_HUMAN	-----WN	KEMGDHL-VK	HGDGVKDIAF	EVEDCDYIVQ	KARERGA KIM
	HPPD_RAT	-----WN	KEMGDHL-VK	HGDGVKDIAF	EVEDCEHIVQ	KARERGA KIV
	HPPD_PIG	-----WN	KEMGDHL-VK	HGDGVKDIAF	EVEDCDYIVQ	KARERGA IIV
	HPPD_MOUSE	-----WN	KEMGDHL-VK	HGDGVKDIAF	EVEDCDHIVQ	KARERGA KIV
	HPPD_PSESP	-----P	HSVASYFAAE	HGPSVCGMAF	RVKDSQKAYK	RALELGAQPI
	MELA_SHECO	-----K	QGFSAQFAKT	HGPAISSMGW	RVEDANFAFE	GAVARGAKPA
	PEA3_MOUSE	SDEQFVPDFH	---SENLA FH	SPTTRIKKEP	QSPRTDPALS	CSRKPPLPYH
		210	220	230	240	250
40	HPPD_Hv	FAPV-----	-----DLGRG	FAPAEVELYG	--DVVLR FVS	HP--DG--TD
	HPPD_Ath	SPPI-----	-----VLNEA	VTIAEVKLYG	--DVVLR YVS	YKAEDT--EK
	HPPD_HUMAN	REP-----	-WVEQDKFGK	VKFAVLQTYG	--DTTHTLVE	KMN-----YI
	HPPD_RAT	REP-----	-WVEEDKFGK	VKFAVLQTYG	--DTTHTLVE	KIN-----YT
	HPPD_PIG	REEVC-CAAD	VRGHHTPLDR	AR----QVWE	--GT---LVE	KMT-----FC
45	HPPD_MOUSE	REP-----	-WVEQDKFGK	VKFAVLQTYG	--DTTHTLVE	KIN-----YT
	HPPD_PSESP	HI-----	---ETGPME	LNLPAIKGIG	--GAPLYLID	RFEGESSIYD
	MELA_SHECO	AD-----	---EV---KD	LPYPAIYGIG	--DSLIIYFID	TFGDDNNIYT
	PEA3_MOUSE	HGEQCLYSRQ	IAIKSPAPGA	PGQSPLQPF	RAEQQQLLR	ASSSSQSHPG

## 25

	260	270	280	290	300
HPPD_Hv	VPFLPGFEGV	TNPDA-----	VDYGLTRFDH	VVGNVV--EL	-APAAAYIAG
HPPD_Ath	SEFLPGFERV	EDASSF---P	LDYGIRRLDH	AVGNVP--EL	-GPALTYVAG
HPPD_HUMAN	GQFLPGYEAP	AFMDPLLPKL	PKCSLEMIDH	IVGNQPDQEM	-VSASEW---
HPPD_RAT	GRFLPGFEAP	TYKDTLLPKL	PSCNLEIIDH	IVGNQPDQEM	-ESASEW---
5 HPPD_PIG	LDSRPQPSQT	LLHRLLLSKL	PKCGLLEIIDH	IVGNQPDQEM	-ESASQW---
HPPD_MOUSE	GRFLPGFEAP	TYKDTLLPKL	PRCNLEIIDH	IVGNQPDQEM	-QSASEW---
HPPD_PSESP	IDFV--FLEG	VDRHPVGA--	---GLKIIDH	LTHNVYRGRM	-A---YWANF
MELA_SHECO	SDF-----EA	LDEPIITQ--	-EKGFIEVDH	LTNNVHKGTM	-E---YWSNF
PEA3_MOUSE	HGYLGEHSSV	FQQPVMCHS	FTSPQGGGRE	PLPAPYQHQL	SEPCPPYPQO
	310	320	330	340	350
10 HPPD_Hv	FT---GFHEF	AEFTAEDVGT	TESGLNSVVL	ANNSEGVLLP	LINEPVHGTR
HPPD_Ath	FT---GFHQF	AEFTADDVGT	AESGLNSAVL	ASNDEMULLP	INEPVHGTR
HPPD_HUMAN	YLKNLQFHRF	WSVDDTQVHT	EYSSLRSIVV	ANYEESIKMP	INEPAPG-KK
HPPD_RAT	YLKNLQFHRF	WSVDDTQVHT	EYSSLRSIVV	ANYEESIKMP	INEPAPG-RK
HPPD_PIG	YMRNLQFHRF	WSVDDTQIHT	EYSALRSVVM	ANYEESIKMP	INEPAPG-KK
15 HPPD_MOUSE	YLKNLQFHRF	WSVDDTQVHT	EYSSLRSIVV	TNYEESIKMP	INEPAPG-RK
HPPD_PSESP	YEKLFNFREI	RYF---DIKG	EYTGLTSKAM	TAPDGMIRIP	INE--ESSKG
MELA_SHECO	YKDIFGFTEV	RYF---DIKG	SQTALISYAL	RSPDGSFCIP	INE--GKGDD
PEA3_MOUSE	NFKQ-EYHDP	LYEQAGQPAS	SQGGVSGHRY	PGAGVVIKQE	RTDFAYDSDV
	360	370	380	390	400
20 HPPD_Hv	RSQIQTFLEH	HGGPGVQH-I	AVASSDVLRT	LRKMRARSAM	GGFDFLPPPL
HPPD_Ath	KSQIQTYLEH	NEGAGLQH-L	ALMSIEDIFRT	LREMRKRSSI	GGFDFMPSP
HPPD_HUMAN	KSQIQEYVDY	NGGAGVQH-I	ALKTEDIIITA	IRHLRER---	-GLEFLSVP-
HPPD_RAT	KSQIQEYVDY	NGGAGVQH-I	ALRTEDIITT	IRHLRER---	-GMEFLAVP-
HPPD_PIG	KSQIQEYVDY	NGGAGVQH-I	ALKTEDIIITA	IRSLRER---	-GVEFLAVP-
HPPD_MOUSE	KSQIQEYVDY	NGGAGVQH-I	ALKTEDIIITA	IRHLRER---	-GTEFLAAP-
25 HPPD_PSESP	AGQIEEFLMQ	FNGEGIQH-V	AFLSDDLKT	WDHLKSI---	-GMRFTAPP
MELA_SHECO	RNQIDEYLKE	YDGPVQH-L	AFRSRDIVAS	LDAMEGS---	-SIQTLDIIP
PEA3_MOUSE	PGCASMYLHP	EGFSGSPGD	GVMGYGYEKS	LRPFPDDVCI	VPKKFEGDIK
	410	420	430	440	450
30 HPPD_Hv	PKYYEGVRR	AGD--VLSEA	QIKECQELGV	LVDRDDQG--	---VLL-----
HPPD_Ath	PTYYQNLKKR	VGD--VLSDD	QIKECEELGI	LVDRDDQG--	---TLL-----
HPPD_HUMAN	STYYQLREK	LKTAKIKVKE	NIDALEELKI	LVDDYDEKG--	---YLL-----
HPPD_RAT	SSYYRLLEN	LKTSKIQVKE	NMDVLEELKI	LVDDYDEKG--	---YLL-----
HPPD_PIG	FTYYKQLQEK	LKSAKIRVKE	SIDVLEELKI	LVDDYDEKG--	---YLL-----
HPPD_MOUSE	SSYYKLLREN	LKSAKIQVKE	SMDVLEELHI	LVDDYDEKG--	---YLL-----
HPPD_PSESP	DTYYEMLEGR	LPN----HGE	PVGELQARGI	LLDGSSSESGD	KRLLL-----
35 MELA_SHECO	E-YYDTIFEK	LPQ----VTE	DRDRIKHQI	LVDDGEDG--	---YLL-----
PEA3_MOUSE	QEGIGAFREG	PPYQR-----	-RGALQLWQF	LVALLDPTN	AHFIAWTGRG
	460	470	480	490	500
HPPD_Hv	QIFTKPVGDR	PTLFLEMIQR	IGCMKDERG	EE----YQKG	GCGGFGKGNF
HPPD_Ath	QIFTKPLGDR	PTIFIEIIQR	VGCMKDEEG	KA----YQSG	GCGGFGKGNF
40 HPPD_HUMAN	QIFTKPVQDR	PTLFLEVIQR	NNHQ-----	-----	---GFGAGNF
HPPD_RAT	QIFTKPMQDR	PTLFLEVIQR	NNHQ-----	-----	---GFGAGNF
HPPD_PIG	QIFTKPMQDR	PTVFLEVIQR	NNHQ-----	-----	---GFGAGNF
HPPD_MOUSE	QIFTKPMQDR	PTLFLEVIQR	NNHQ-----	-----	---GFGAGNF
HPPD_PSESP	QIFSETLMGP	---VFFEFIQR	-----KGDD-	-----	---GFGEGNF
MELA_SHECO	QIFTKNLFGP	---IFIEIIQR	-----KNNL-	-----	---GFGEGNF
45 PEA3_MOUSE	MEFKLIEPEE	VARLWGIQKN	RPAMNYDKLS	RSLRYYYYEK	IMQKVAGERY
	510	520	530	540	550
HPPD_Hv	-----SE	LFK-SIE-DY	---EKS---LEA	KQSAAV-QGS	

## 26

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HPPD_Ath      -----SE LFK-SIE-EY --EKT--LEA KQLVG
HPPD_HUMAN    -----NS LFK-AFEEEEQ --NLRGNLTN METNGVVPGM
HPPD_RAT      -----NS LFK-AFEEEEQ --ALRG
HPPD_PIG      -----NS LFK-AFEEEEQ --ELRGNLTD TDPNGVPPRL
HPPD_MOUSE    -----NS LFK-AFEEEEQ --ALRGNLTD LEPNGVVRSGM
5 HPPD_PSESP   -----KA LFE-SIERDQ --VRRGVLST -D
MELA_SHECO    -----KA LFE-SIERDQ --VRRGVL
PEA3_MOUSE    VYKFVCEPEA LFSLAFFDNQ RPALKAEFDR PVSEEDTVPL SHLDESPAYL

```

560

570

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10 HPPD_Hv
HPPD_Ath
HPPD_HUMAN
HPPD_RAT
HPPD_PIG
HPPD_MOUSE
HPPD_PSESP
15 MELA_SHECO
PEA3_MOUSE      PELTGPAPPF GHRGGYSY

```

Key:

20 HPPD\_Hv: *Hordeum vulgare* 4-hydroxyphenylpyruvate  
dioxxygenase (HvSD36)

HPPD\_Ath: *Arabidopsis thaliana*  
4-hydroxyphenylpyruvate dioxxygenase

HPPD\_HUMAN: *H.sapiens* 4-hydroxyphenylpyruvate  
dioxxygenase

HPPD\_PIG: pig 4-hydroxyphenylpyruvate dioxxygenase

HPPD\_RAT: rat F alloantigen

25 HPPD\_MOUSE: mouse 4-hydroxyphenylpyruvate  
dioxxygenase

MELA\_SHECO: *S. colwelliana* mela protein

HPPD\_PSESP: *Pseudomonas* sp. (strain P.J.874)  
4-hydroxyphenylpyruvate dioxxygenase

30 PEA3\_MOUSE: *Mus musculus* (mouse) PEA3 polypeptide

35 The greatest homology was with the *Arabidopsis* sequence,  
viz. 58% over the entire sequence (62% over 412 amino  
acids), followed by HPPD\_RAT with 35% (over 365 amino  
acids), HPPD\_HUMAN 34% (over 365 amino acids), HPPD\_MOUSE  
34% (over 371 amino acids).

## Example 4

Raising barley (*Hordeum vulgare*)

40 Barley seedlings (*Hordeum vulgare* L. cv. Carina, Ackermann  
Saatzucht, Irbach, Germany) were raised over a period of 15 days  
under controlled conditions in a controlled-environment cabinet  
in so-called Mitscherlich pots in soil containing 4 g of Osmocote  
45 5M (Urania, Hamburg, Germany) per liter. To ensure uniform  
growth, the seeds were germinated on moist filter paper in the  
dark for 2 days at 4°C and 1 day at 21°C, and only those seedlings

were planted which showed the same longitudinal growth of the primary root. After these seedlings had been transferred onto soil, they were covered with screened soil to a depth of 1.5 cm. Thereafter, the plants were incubated for 9 days at 16 hours light 5 (120  $\mu\text{m}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$ ) and 8 hours darkness in conjunction with a temperature shift (21°C during the day, 16°C during the night). After 9 days, the plants were kept for 2 days (days 10 and 11) in the dark at the abovementioned temperature in order to induce senescence.

10

## Example 5

## Raising tobacco

The tobacco plants were raised following the known method. The 15 tobacco cultivar used is *Nicotiana tabacum* cv. Xanthi.

## Example 6

## Transformation of tobacco

20 The expression cassette according to the invention comprising the HPPD gene with Sequence 1 was cloned into vector pBinAR-Hyg (Fig. 4). Tobacco plants as described in Example 5 were subsequently transformed with this vector following the known method.

25

## Example 7

## Increasing the tocopherol biosynthesis in tobacco

The HPPD cDNA was provided with a CaMV 35S promoter and 30 overexpressed in tobacco using the 35S promoter. In parallel, the seed-specific phaseolin gene promoter was used to increase the tocopherol content specifically in the tobacco seed. Tobacco plants which had been transformed with the relevant constructs were raised in the greenhouse. The  $\alpha$ -tocopherol content of the 35 total plant and of the seeds of the plant was subsequently determined. In all cases, the  $\alpha$ -tocopherol concentration was increased in comparison with the untransformed plant.

40

45

## SEQUENCE PROTOCOL

## (1) GENERAL INFORMATION

## (i) APPLICANT

(A) NAME: BASF AG  
 (B) STREET: Carl Bosch  
 (C) TOWN: Ludwigshafen  
 (D) FEDERAL COUNTRY: Germany  
 (F) POSTCODE: 67056  
 (G) TELEPHONE: 0621-60-52698

(ii) TITLE OF APPLICATION: HPPD sequence from  
 barley

(iii) NUMBER OF SEQUENCES: 2

(iv) COMPUTER-READABLE FORM:

(A) RECORDING MEDIUM: floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: PatentIn release #1.0, Version  
 #1.25 (EPA)

## (2) INFORMATION ON SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1565 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETIC: NO

(iii) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: hppd from barley  
 (D) DEVELOPMENTAL STAGE: senescence

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: lambda FIXII library of barley  
 (B) CLONE: pHvSD36.seq

(ix) FEATURES:

(A) NAME/KEY: CDS  
 (B) POSITION: 9..1313

(x) PUBLICATION DETAILS:

(A) AUTHORS: Krupinska, Karin  
 (B) TITLE: Overexpression of HPPD  
 (C) JOURNAL: overexpression of HPPD  
 (G) DATE: 1998  
 (K) RELEVANT RESIDUES IN SEQ ID NO: 1 FROM 1  
 TO 1565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGCACACC ATG CCG CCC ACC CCC ACC ACC CCC GCG GCT ACC GGC GCC GCC  
 Met Pro Pro Thr Pro Thr Thr Pro Ala Ala Thr Gly Ala Ala

1

5

10

## 29

GCC	GCG	GTG	ACG	CCG	GAG	CAC	GCG	CGA	CCG	CAC	CGA	ATG	GTC	CGC	TTC	98
Ala	Ala	Val	Thr	Pro	Glu	His	Ala	Arg	Pro	His	Arg	Met	Val	Arg	Phe	
15					20				25						30	
AAC	CCG	CGC	AGC	GAC	CGC	TTC	CAC	ACG	CTC	TCC	TTC	CAC	CAC	GTC	GAG	146
Asn	Pro	Arg	Ser	Asp	Arg	Phe	His	Thr	Leu	Ser	Phe	His	His	Val	Glu	
				35					40					45		
TTC	TGG	TGC	GCG	GAC	GCC	GCC	TCC	GCC	GCC	GGC	CGC	TTC	GCG	TTC	GCG	194
Phe	Trp	Cys	Ala	Asp	Ala	Ala	Ser	Ala	Ala	Gly	Arg	Phe	Ala	Phe	Ala	
			50					55					60			
CTC	GGC	GCG	CCG	CTC	GCC	GCC	AGG	TCC	GAC	CTC	TCC	ACG	GGG	AAC	TCC	242
Leu	Gly	Ala	Pro	Leu	Ala	Ala	Arg	Ser	Asp	Leu	Ser	Thr	Gly	Asn	Ser	
		65					70					75				
GCG	CAC	GCC	TCC	CAG	CTG	CTC	CGC	TCG	GGC	TCC	CTC	GCC	TTC	CTC	TTC	290
Ala	His	Ala	Ser	Gln	Leu	Leu	Arg	Ser	Gly	Ser	Leu	Ala	Phe	Leu	Phe	
	80					85					90					
ACC	GCG	CCC	TAC	GCC	AAC	GGC	TGC	GAC	GCC	GCC	ACC	GCC	TCC	CTG	CCC	338
Thr	Ala	Pro	Tyr	Ala	Asn	Gly	Cys	Asp	Ala	Ala	Thr	Ala	Ser	Leu	Pro	
95					100				105						110	
TCC	TTC	TCC	GCC	GAC	GCC	GCG	CGC	CGG	TTC	TCC	GCC	GAC	CAC	GGG	ATC	386
Ser	Phe	Ser	Ala	Asp	Ala	Ala	Arg	Arg	Phe	Ser	Ala	Asp	His	Gly	Ile	
				115					120					125		
GCG	GTG	CGC	TCC	GTA	GCG	CTG	CGC	GTC	GCA	GAC	GCC	GCC	GAG	GCC	TTC	434
Ala	Val	Arg	Ser	Val	Ala	Leu	Arg	Val	Ala	Asp	Ala	Ala	Glu	Ala	Phe	
			130					135					140			
CGC	GCC	AGT	CGT	CGA	CGG	GGC	GCG	CGC	CCG	GCC	TTC	GCC	CCC	GTG	GAC	482
Arg	Ala	Ser	Arg	Arg	Arg	Gly	Ala	Arg	Pro	Ala	Phe	Ala	Pro	Val	Asp	
		145					150					155				
CTC	GGC	CGC	GGC	TTC	GCG	TTC	GCG	GAG	GTC	GAG	CTC	TAC	GGC	GAC	GTC	530
Leu	Gly	Arg	Gly	Phe	Ala	Phe	Ala	Glu	Val	Glu	Leu	Tyr	Gly	Asp	Val	
	160					165					170					
GTG	CTC	CGC	TTC	GTC	AGC	CAC	CCG	GAC	GGC	ACG	GAC	GTG	CCC	TTC	TTG	578
Val	Leu	Arg	Phe	Val	Ser	His	Pro	Asp	Gly	Thr	Asp	Val	Pro	Phe	Leu	
175					180				185						190	
CCG	GGG	TTC	GAG	GGC	GTA	ACC	AAC	CCG	GAC	GCC	GTG	GAC	TAC	GGC	CTG	626
Pro	Gly	Phe	Glu	Gly	Val	Thr	Asn	Pro	Asp	Ala	Val	Asp	Tyr	Gly	Leu	
				195					200					205		
ACG	CGG	TTC	GAC	CAC	GTC	GTC	GGC	AAC	GTC	CCG	GAG	CTT	GCC	CCC	GCC	674
Thr	Arg	Phe	Asp	His	Val	Val	Gly	Asn	Val	Pro	Glu	Leu	Ala	Pro	Ala	
			210					215					220			



## 30

GCA	GCC	TAC	ATC	GCC	GGG	TTC	ACG	GGG	TTC	CAC	GAG	TTC	GCC	GAG	TTC	722
Ala	Ala	Tyr	Ile	Ala	Gly	Phe	Thr	Gly	Phe	His	Glu	Phe	Ala	Glu	Phe	
		225					230					235				
ACG	GCG	GAG	GAC	GTG	GGC	ACG	ACC	GAG	AGC	GGG	CTC	AAC	TCG	GTG	GTG	770
Thr	Ala	Glu	Asp	Val	Gly	Thr	Thr	Glu	Ser	Gly	Leu	Asn	Ser	Val	Val	
	240					245					250					
CTC	GCC	AAC	AAC	TCG	GAG	GGC	GTG	CTG	CTG	CCG	CTC	AAC	GAG	CCG	GTG	818
Leu	Ala	Asn	Asn	Ser	Glu	Gly	Val	Leu	Leu	Pro	Leu	Asn	Glu	Pro	Val	
255					260					265					270	
CAC	GGC	ACC	AAG	CGC	CGG	AGC	CAG	ATA	CAG	ACG	TTC	CTG	GAA	CAC	CAC	866
His	Gly	Thr	Lys	Arg	Arg	Ser	Gln	Ile	Gln	Thr	Phe	Leu	Glu	His	His	
			275						280					285		
GGC	GGC	CCG	GGC	GTG	CAG	CAC	ATC	GCG	GTG	GCC	AGC	AGT	GAC	GTG	CTC	914
Gly	Gly	Pro	Gly	Val	Gln	His	Ile	Ala	Val	Ala	Ser	Ser	Asp	Val	Leu	
		290						295					300			
AGG	ACG	CTC	AGG	AAG	ATG	CGT	GCG	CGC	TCC	GCC	ATG	GGC	GGC	TTC	GAC	962
Arg	Thr	Leu	Arg	Lys	Met	Arg	Ala	Arg	Ser	Ala	Met	Gly	Gly	Phe	Asp	
		305					310					315				
TTC	CTG	CCA	CCC	CCG	CTG	CCG	AAG	TAC	TAC	GAA	GGC	GTG	CGA	CGC	CTT	1010
Phe	Leu	Pro	Pro	Pro	Leu	Pro	Lys	Tyr	Tyr	Glu	Gly	Val	Arg	Arg	Leu	
	320					325					330					
GCC	GGG	GAT	GTC	CTC	TCG	GAG	GCG	CAG	ATC	AAG	GAA	TGC	CAG	GAG	CTG	1058
Ala	Gly	Asp	Val	Leu	Ser	Glu	Ala	Gln	Ile	Lys	Glu	Cys	Gln	Glu	Leu	
335					340					345					350	
GGT	GTG	CTC	GTC	GAT	AGG	GAC	GAC	CAA	GGG	GTG	TTG	CTC	CAA	ATC	TTC	1106
Gly	Val	Leu	Val	Asp	Arg	Asp	Asp	Gln	Gly	Val	Leu	Leu	Gln	Ile	Phe	
				355					360					365		
ACC	AAG	CCA	GTA	GGG	GAC	AGG	CCG	ACC	TTG	TTC	CTG	GAG	ATG	ATC	CAG	1154
Thr	Lys	Pro	Val	Gly	Asp	Arg	Pro	Thr	Leu	Phe	Leu	Glu	Met	Ile	Gln	
		370						375					380			
AGG	ATC	GGG	TGC	ATG	GAG	AAG	GAC	GAG	AGA	GGG	GAA	GAG	TAC	CAG	AAG	1202
Arg	Ile	Gly	Cys	Met	Glu	Lys	Asp	Glu	Arg	Gly	Glu	Glu	Tyr	Gln	Lys	
		385					390					395				
GGT	GGC	TGC	GGC	GGG	TTC	GGC	AAA	GGC	AAC	TTC	TCC	GAG	CTG	TTC	AAG	1250
Gly	Gly	Cys	Gly	Gly	Phe	Gly	Lys	Gly	Asn	Phe	Ser	Glu	Leu	Phe	Lys	
	400					405					410					
TCC	ATT	GAA	GAT	TAC	GAG	AAG	TCC	CTT	GAA	GCC	AAG	CAA	TCT	GCT	GCA	1298
Ser	Ile	Glu	Asp	Tyr	Glu	Lys	Ser	Leu	Glu	Ala	Lys	Gln	Ser	Ala	Ala	
415					420					425					430	

31

GTT CAG GGA TCA TAGGATAGAA GCTGGTCCTT GTATCATGGT CTCATGGAGC 1350  
Val Gln Gly Ser

435

AAAAGAAAAC AATGTTGTTT GTAATATGCG TCGCACAATT ATATCAATGT TATAATTGGT 1410

GAAGCTGAAG ACAGATGTAT CCTATGTATG ATGGGTGTAA TGGATGGTAG AGGGGCTCAC 1470

ACATGAAGAA AATGTAGCGT TGACATTGTT GTACAATCTT GCTTGCAAGT AAAATAAAGA 1530

ACAGATTTTG AGTTCTGCAA AAAAAAAAAA AAAAA 1565

## (2) INFORMATION ON SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) TYPE OF MOLECULE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Pro Pro Thr Pro Thr Thr Pro Ala Ala Thr Gly Ala Ala Ala Ala  
1 5 10 15

Val Thr Pro Glu His Ala Arg Pro His Arg Met Val Arg Phe Asn Pro  
20 25 30

Arg Ser Asp Arg Phe His Thr Leu Ser Phe His His Val Glu Phe Trp  
35 40 45

Cys Ala Asp Ala Ala Ser Ala Ala Gly Arg Phe Ala Phe Ala Leu Gly  
50 55 60

Ala Pro Leu Ala Ala Arg Ser Asp Leu Ser Thr Gly Asn Ser Ala His  
65 70 75 80

Ala Ser Gln Leu Leu Arg Ser Gly Ser Leu Ala Phe Leu Phe Thr Ala  
85 90 95

Pro Tyr Ala Asn Gly Cys Asp Ala Ala Thr Ala Ser Leu Pro Ser Phe  
100 105 110

Ser Ala Asp Ala Ala Arg Arg Phe Ser Ala Asp His Gly Ile Ala Val  
115 120 125

Arg Ser Val Ala Leu Arg Val Ala Asp Ala Ala Glu Ala Phe Arg Ala  
130 135 140

Ser Arg Arg Arg Gly Ala Arg Pro Ala Phe Ala Pro Val Asp Leu Gly  
145 150 155 160

## 32

Arg Gly Phe Ala Phe Ala Glu Val Glu Leu Tyr Gly Asp Val Val Leu  
 165 170 175  
 Arg Phe Val Ser His Pro Asp Gly Thr Asp Val Pro Phe Leu Pro Gly  
 180 185 190  
 Phe Glu Gly Val Thr Asn Pro Asp Ala Val Asp Tyr Gly Leu Thr Arg  
 195 200 205  
 Phe Asp His Val Val Gly Asn Val Pro Glu Leu Ala Pro Ala Ala Ala  
 210 215 220  
 Tyr Ile Ala Gly Phe Thr Gly Phe His Glu Phe Ala Glu Phe Thr Ala  
 225 230 235 240  
 Glu Asp Val Gly Thr Thr Glu Ser Gly Leu Asn Ser Val Val Leu Ala  
 245 250 255  
 Asn Asn Ser Glu Gly Val Leu Leu Pro Leu Asn Glu Pro Val His Gly  
 260 265 270  
 Thr Lys Arg Arg Ser Gln Ile Gln Thr Phe Leu Glu His His Gly Gly  
 275 280 285  
 Pro Gly Val Gln His Ile Ala Val Ala Ser Ser Asp Val Leu Arg Thr  
 290 295 300  
 Leu Arg Lys Met Arg Ala Arg Ser Ala Met Gly Gly Phe Asp Phe Leu  
 305 310 315 320  
 Pro Pro Pro Leu Pro Lys Tyr Tyr Glu Gly Val Arg Arg Leu Ala Gly  
 325 330 335  
 Asp Val Leu Ser Glu Ala Gln Ile Lys Glu Cys Gln Glu Leu Gly Val  
 340 345 350  
 Leu Val Asp Arg Asp Asp Gln Gly Val Leu Leu Gln Ile Phe Thr Lys  
 355 360 365  
 Pro Val Gly Asp Arg Pro Thr Leu Phe Leu Glu Met Ile Gln Arg Ile  
 370 375 380  
 Gly Cys Met Glu Lys Asp Glu Arg Gly Glu Glu Tyr Gln Lys Gly Gly  
 385 390 395 400  
 Cys Gly Gly Phe Gly Lys Gly Asn Phe Ser Glu Leu Phe Lys Ser Ile  
 405 410 415  
 Glu Asp Tyr Glu Lys Ser Leu Glu Ala Lys Gln Ser Ala Ala Val Gln  
 420 425 430  
 Gly Ser

We claim:

1. The DNA sequence SEQ ID NO:1 and DNA sequences hybridizing  
5 therewith, encoding an HPPD.
2. An expression cassette comprising a promoter and a DNA  
sequence as claimed in claim 1.
- 10 3. An expression cassette as claimed in claim 2, comprising the  
CaMV 35S promoter.
4. An expression cassette as claimed in claim 2, comprising the  
seed-specific phaseolin promoter.
- 15 5. An expression cassette as claimed in claim 2, the DNA  
sequence as claimed in claim 1 being functionally linked to  
another protein in such a way that a joint translation  
product is formed.
- 20 6. The use of the expression cassette as claimed in claim 2 for  
transforming plants.
7. A method of transforming a plant, which comprises introducing  
25 an expression cassette as claimed in claim 2 into a plant  
cell, into callus tissue, into an entire plant or into plant  
cell protoplasts.
8. A method of transforming plants, which comprises  
30
  - 1) transferring the expression cassette as claimed in  
claim 2 into an agrobacterial strain,
  - 2) isolating the recombinant clones formed, and
  - 3) using the latter for transforming plants.
- 35 9. A method as claimed in claim 8, the transformation being  
accomplished with the aid of the strain *Agrobacterium*  
*tumefaciens*.
- 40 10. A method of transforming plants as claimed in claim 7,  
wherein the transformation is accomplished with the aid of  
electroporation.
11. A method of transforming plants as claimed in claim 7,  
45 wherein the transformation is accomplished with the aid of  
the particle bombardment method.

## 34

12. A plant with an elevated vitamin E content, comprising an expression cassette as claimed in any one of claims 2 to 5.
13. A plant as claimed in claim 12, selected from the group consisting of soya, barley, oats, wheat, oilseed rape, maize or sunflowers.
14. A method of generating plants with an elevated vitamin E content, which comprises expressing, in plants, a DNA sequence as claimed in claim 1.
15. A method as claimed in claim 14, wherein the DNA sequence is expressed in a tobacco plant.
16. A method as claimed in any of claims 14 and 15, wherein expression takes place in the leaves or the seeds of the plant.
17. The use of an expression cassette as claimed in any of claims 2 to 5 for generating plants with an elevated vitamin E content by means of expressing, in plants, a DNA sequence as claimed in claim 1.
18. The use of the expression cassette as claimed in claim 2 for generating a test system for identifying HPPD inhibitors.
19. A test system based on the expression of an expression cassette as claimed in claim 2 for identifying HPPD inhibitors.
20. A herbicidally active substance which can be identified by means of a test system as claimed in claim 19.
21. The use of a plant as claimed in claim 12 for generating plant HPPD.
22. The use of the expression cassette as claimed in claim 2 for generating plants with elevated resistance to HPPD inhibitors by means of higher expression of a DNA sequence as claimed in claim 1.
23. A method of generating plants with elevated resistance to HPPD inhibitors by means of higher expression of a DNA sequence as claimed in claim 1.

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24. A plant with elevated resistance to HPPD inhibitors,  
comprising an expression cassette as claimed in any of claims  
2 to 5.

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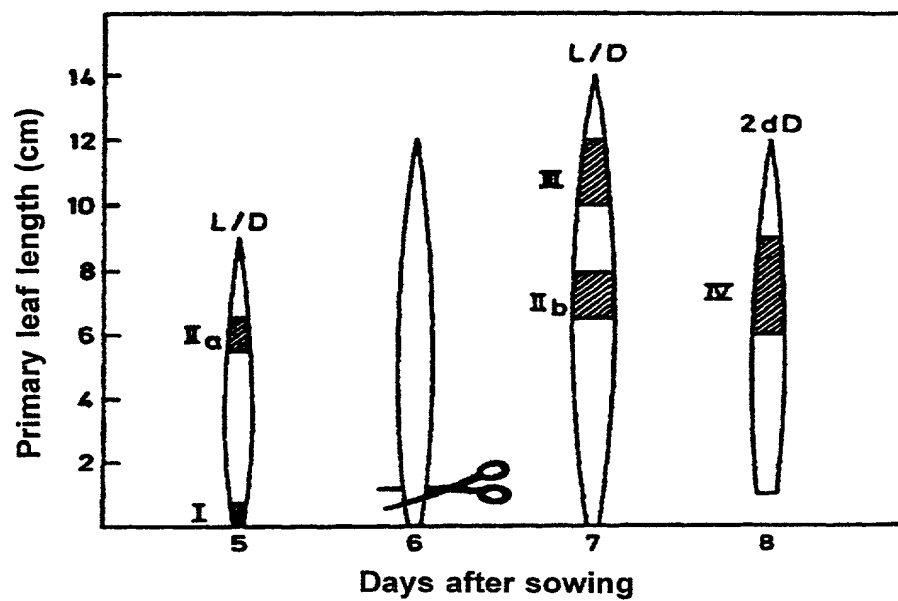
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Fig. 1/7



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Fig. 2/7

I IIa IIb III IV

3100 nt →

1600 nt →





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Fig. 3/7

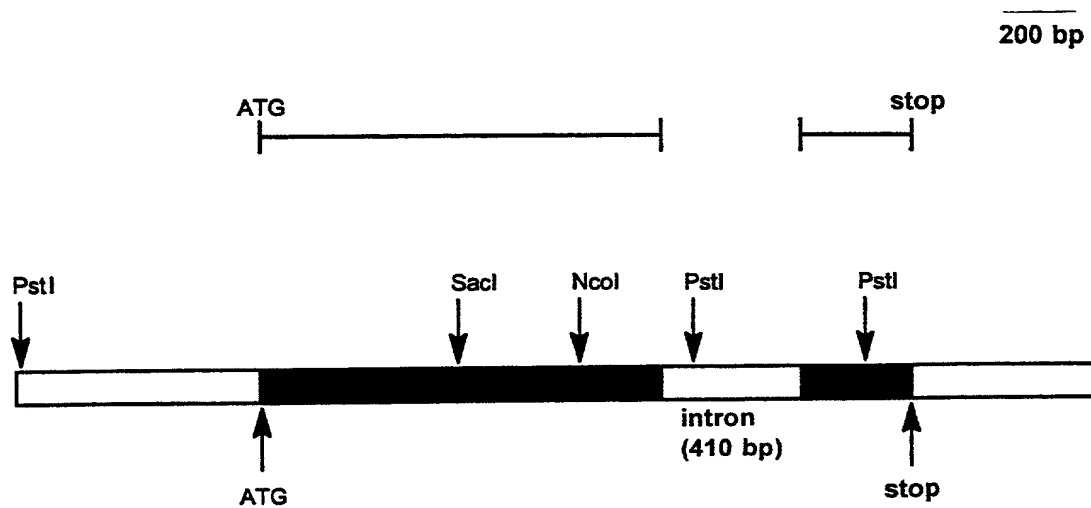
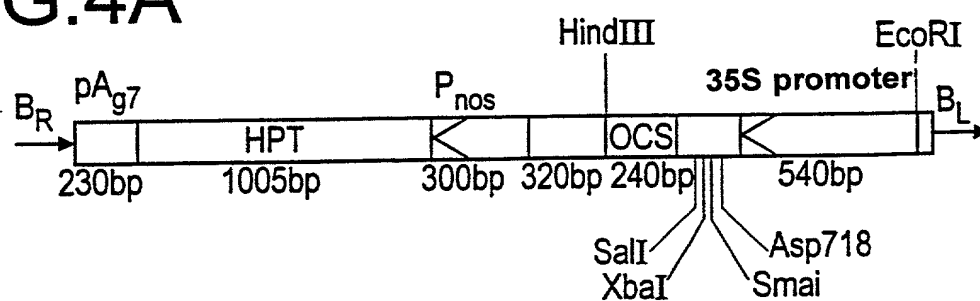
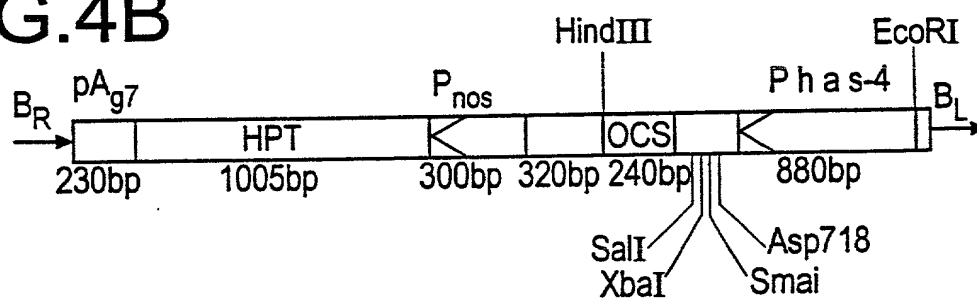


Fig. 4/7

## FIG.4A



## FIG.4B



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Fig. 5/7



**A. Model**      **B. Field**

9    10   11   12      29.5.    $\xrightarrow{\quad\quad\quad}$    21.6.

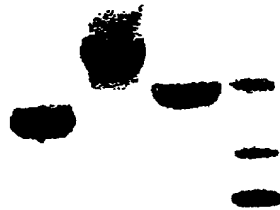
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**HvSD36**      - 1.6 kb

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Fig. 7/7

B E H X



DNA sequence encoding a hydroxyphenylpyruvate dioxygenase gene  
and its overproduction in plants

## 5 Abstract

A method is described of generating plants with elevated vitamin E  
biosynthesis performance by overexpressing a plant HPPD gene from  
barley.

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# Declaration, Power of Attorney

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0050/048141

We (I), the undersigned inventor(s), hereby declare(s) that:

My residence, post office address and citizenship are as stated below next to my name,

We (I) believe that we are (I am) the original, first, and joint (sole) inventor(s) of the subject matter which is claimed and for which a patent is sought on the invention entitled

DNA sequence encoding a hydroxyphenylpyruvate dioxygenase, and its overproduction in plants

the specification of which

☒ is attached hereto.

☐ was filed on \_\_\_\_\_ as

Application Serial No. \_\_\_\_\_

and amended on \_\_\_\_\_.

☒ was filed as PCT international application

Number PCT/EP 98/03832

on 23/06/1998

and was amended under PCT Article 19

on \_\_\_\_\_ (if applicable).

We (I) hereby state that we (I) have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

We (I) acknowledge the duty to disclose information known to be material to the patentability of this application as defined in Section 1.56 of Title 37 Code of Federal Regulations.

We (I) hereby claim foreign priority benefits under 35 U.S.C. § 119(a)–(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed. Prior Foreign Application(s)

Application No.	Country	Day/Month/Year	Priority Claimed
19730066.9	Germany	14.JULI 1997	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No

pdusket001 - 25

We (I) hereby claim the benefit under Title 35, United States Codes, § 119(e) of any United States provisional application(s) listed below.

\_\_\_\_\_  
(Application Number)

\_\_\_\_\_  
(Filing Date)

\_\_\_\_\_  
(Application Number)

\_\_\_\_\_  
(Filing Date)

We (I) hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s), or § 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR § 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

**Application Serial No.**

**Filing Date**

**Status (pending, patented,  
abandoned)**

_____	_____	_____
_____	_____	_____
_____	_____	_____
_____	_____	_____

And we (I) hereby appoint **Messrs. HERBERT. B. KEIL**, Registration Number 18,967; and **RUSSEL E. WEINKAUF**, Registration Number 18,495; the address of both being Messrs. Keil & Weinkauf, 1101 Connecticut Ave., N.W., Washington, D.C. 20036 (telephone 202-659-0100), our attorneys, with full power of substitution and revocation, to prosecute this application, to make alterations and amendments therein, to sign the drawings, to receive the patent, and to transact all business in the Patent Office connected therewith.

We (I) declare that all statements made herein of our (my) own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.



*1/00*  
Harald Seulberger  
NAME OF INVENTOR

Harald Seulberger  
Signature of Inventor

Date

09/07/1998

Speyerer Wingert 25  
67141 Neuhofen *DER*  
Germany  
Citizen of: Germany  
Post Office Address: same as residence

*2/00*  
Jens Lerchl  
NAME OF INVENTOR

Jens Lerchl  
Signature of Inventor

Date

09/07/1998

Im Steg 36  
68526 Ladenburg *DER*  
Germany  
Citizen of: Germany  
Post Office Address: same as residence

*3/00*  
Ralf-Michael Schmidt  
NAME OF INVENTOR

Ralf-Michael Schmidt  
Signature of Inventor

Date

09/07/1998

Am Schloßgarten 9 d  
67489 Kirrweiler *DER*  
Germany  
Citizen of: Germany  
Post Office Address: same as residence

*4/00*  
Karin Krupinska  
NAME OF INVENTOR

Karin Krupinska  
Signature of Inventor

Date

27/07/1998

Gyrhofstr. 15  
50931 Koeln *DER*  
Germany  
Citizen of: Germany  
Post Office Address: same as residence

0050/048141

**Declaration**

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h-w

Jon Falk  
NAME OF INVENTOR

J. Falk  
Signature of Inventor

Date

27/07/1998

Feldhuhnweg 23  
50127 Bergheim/Quadrath DE  
Germany  
Citizen of: Germany  
Post Office Address: same as residence

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